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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/142,108B

DATE: 09/19/2001

TIME: 10:35:15

Input Set : A:\11658.bk1

Output Set: N:\CRF3\09192001\I142108B.raw

4 <110> APPLICANT: Brugliera, Filippa
 5 Holton, Timothy A.
 6 Michael, Michael Z.
 8 <120> TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
 9 AND USES THEREFOR
 11 <130> FILE REFERENCE: 11658
 13 <140> CURRENT APPLICATION NUMBER: 09/142,108B
 C--> 14 <141> CURRENT FILING DATE: 2001-08-30
 16 <150> PRIOR APPLICATION NUMBER: PN8386
 17 <151> PRIOR FILING DATE: 1996-03-01
 19 <160> NUMBER OF SEQ ID NOS: 45
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1789
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Petunia x hybrida
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (50)..(1588)
 32 <400> SEQUENCE: 1
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 34 Met Glu Ile
 35 1
 37 tta agc cta att ctg tac acc gtc att ttc tca ttt ctt cta caa ttc 106
 38 Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe
 39 5 10 15
 41 att ctt aga tca ttt ttc cgt aaa cgt tac cct tta cca tta cca cca 154
 42 Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro
 43 20 25 30 35
 45 ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202
 46 Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
 47 40 45 50
 49 aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250
 50 Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu
 51 55 60 65
 53 atg tat ctt aag atg ggg ttc gta gac gtg gtg gtt gca gcc tcg gca 298
 54 Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
 55 70 75 80
 57 tcg gtt gca gct cag ttc ttg aaa act cat gat gct aat ttc tcg agc 346
 58 Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser Ser
 59 85 90 95
 61 cgt cca cca aat tct ggt gca gaa cat atg gct tat aat tat cag gat 394
 62 Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln Asp
 63 100 105 110 115
 65 ctt gtt ttt gca cct tat gga cct aga tgg cgt atg ctt agg aaa att 442
 66 Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile
 67 120 125 130

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70 Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His
71          135          140          145
73 gtc cgc cag gat gaa gtg aaa aca ctg acg cgc gca cta gca agt gca 538
74 Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser Ala
75          150          155          160
77 ggc caa aag cca gtc aaa tta ggt cag tta ttg aac gtg tgc acg acg 586
78 Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr
79          165          170          175
81 aac gca ctc gcg cga gta atg cta ggt aag cga gta ttt gcc gac gga 634
82 Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp Gly
83 180          185          190          195
85 agt ggc gat gtt gat cca caa gcg gcg gag ttc aag tca atg gtg gtg 682
86 Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val
87          200          205          210
89 gaa atg atg gta gtc gcc ggt gtt ttt aac att ggt gat ttt att ccg 730
90 Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp Phe Ile Pro
91          215          220          225
93 caa ctt aat tgg tta gat att caa ggt gta gcc gct aaa atg aag aag 778
94 Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys Met Lys Lys
95          230          235          240
97 ctc cac gcg cgt ttc gac gcg ttc ttg act gat ata ctt gaa gag cat 826
98 Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu Glu Glu His
99          245          250          255
101 aag ggt aaa att ttt gga gaa atg aaa gat ttg ttg agt act ttg atc 874
102 Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser Thr Leu Ile
103 260          265          270          275
105 tct ctt aaa aat gat gat gcg gat aat gat gga ggg aaa ctc act gat 922
106 Ser Leu Lys Asn Asp Ala Asp Asn Asp Gly Gly Lys Leu Thr Asp
107          280          285          290
109 aca gaa att aaa gca tta ctt ttg aac ttg ttt gta gct gga aca gac 970
110 Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala Gly Thr Asp
111          295          300          305
113 aca tct tct agt aca gtt gaa tgg gcc att gct gag ctt att cgt aat 1018
114 Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn
115          310          315          320
117 cca aaa ata cta gcc caa gcc cag caa gag atc gac aaa gtc gtt gga 1066
118 Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys Val Val Gly
119          325          330          335
121 agg gac cgg cta gtt ggc gaa ttg gac cta gcc caa ttg aca tac ttg 1114
123 Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu Thr Tyr Leu
124 340          345          350          355
126 gaa gct ata gtc aag gaa acc ttt cgg ctt cat cca tca acc cct ctt 1162
127 Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu
128          360          365          370
130 tca ctt cct aga att gca tct gag agt tgt gag atc aat ggc tat ttc 1210
131 Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr Phe
132          375          380          385
134 att cca aaa ggc tca acg ctt ctc ctt aat gtt tgg gcc att gct cgt 1258

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135 Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala Ile Ala Arg
136           390           395           400
138 gat cca aat gca tgg gct gat cca ttg gag ttt agg cct gaa agg ttt 1306
139 Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe
140       405           410           415
142 ttg cca gga ggt gag aag ccc aaa gtt gat gtc cgt ggg aat gac ttt 1354
143 Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly Asn Asp Phe
144 420           425           430           435
146 gaa gtc ata cca ttt gga gct gga cgt agg att tgt gct gga atg aat 1402
147 Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Asn
148           440           445           450
150 ttg ggt ata cgt atg gtc cag ttg atg att gca act tta ata cat gca 1450
151 Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu Ile His Ala
152           455           460           465
154 ttt aac tgg gat ttg gtc agt gga caa ttg ccg gag atg ttg aat atg 1498
155 Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met Leu Asn Met
156       470           475           480
158 gaa gaa gca tat ggg ctg acc tta caa cgg gct gat cca ttg gtt gtg 1546
159 Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro Leu Val Val
160       485           490           495
162 cac cca agg cct cgc tta gaa gcc caa gcg tac att ggg tga 1588
163 His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
164 500           505           510
166 gcagcaacag cccatggaga taacatgagt gttaaagtga tgagtctcca tatcttgttt 1648
168 agtttgttta tgctttggat ttagtagttt ttatatattgat agatcaatgt ttgcattgtc 1708
170 agtaagaata tccgttgctt gtttcattaa ctccaggtgg acaataaaaag aagtaatttg 1768
172 tatgaaaaaa aaaaaaaaaa a 1789
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 512
177 <212> TYPE: PRT
178 <213> ORGANISM: Petunia x hybrida
180 <400> SEQUENCE: 2
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182   1           5           10           15
184 Leu Gln Phe Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro
185           20           25           30
186 Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His
187           35           40           45
188 Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr
189           50           55           60
190 Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala
191 65           70           75           80
192 Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn
193           85           90           95
194 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn
195           100          105          110
196 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu
197       115           120           125
198 Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp

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200 Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu
201 145      150      155      160
202 Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val
203      165      170      175
204 Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
205      180      185      190
206 Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser
207      195      200      205
208 Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
209      210      215      220
210 Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys
211 225      230      235      240
212 Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu
213      245      250      255
214 Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser
215      260      265      270
216 Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys
217      275      280      285
218 Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala
219      290      295      300
220 Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu
221 305      310      315      320
222 Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys
223      325      330      335
224 Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu
225      340      345      350
226 Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser
227      355      360      365
228 Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn
229      370      375      380
230 Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala
231 385      390      395      400
232 Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro
233      405      410      415
234 Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly
235      420      425      430
236 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala
237      435      440      445
238 Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu
239      450      455      460
240 Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met
241 465      470      475      480
242 Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro
243      485      490      495
245 Leu Val Val His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
246 -----500-----505-----510
250 <210> SEQ ID NO: 3
251 <211> LENGTH: 1737

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/142,108B

DATE: 09/19/2001
TIME: 10:35:15

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Output Set: N:\CRF3\09192001\I142108B.raw

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253 <213> ORGANISM: Dianthus caryophyllus
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260 <400> SEQUENCE: 3
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265 aaaaaaaatt ataatgtcac ccttagagggt aactttctac accatagtcc t atg cac 177
266                                     Met His
267                                     1
269 aat ctc tac tac ctc atc acc acc gtc ttc cgc ggc cac caa aaa ccg 225
270 Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro
271         5                10                15
273 ctt cct cca ggg cca cga cca tgg ccc atc gtg gga aac ctc cca cat 273
274 Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His
275         20                25                30
277 atg ggc cag gca ccg cac cag ggc tta gca gcc ctg gcg caa aag tat 321
278 Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr
279 35                40                45                50
281 ggc cct cta ttg tat atg aga ctg ggg tac gtg gac gtt gtt gtg gcc 369
282 Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val Val Ala
283         55                60                65
285 gcc tca gcg tct gta gcg acc cag ttt ctt aag aca cat gac cta aat 417
286 Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp Leu Asn
287         70                75                80
289 ttt tcg agt agg cca ccg aat tcg ggg gct aaa cac att gct tat aac 465
290 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala Tyr Asn
291         85                90                95
293 tat caa gac ctt gtt ttt gca cct tat gga cct aaa tgg cgc atg ctt 513
294 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu
295         100               105               110
297 agg aaa att tgt tcc tta cac atg ttt tct tct aag gct ttg gac gat 561
298 Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp
299 115               120               125               130
301 ttt aga ctt gtc cgt cag gaa gaa gta tct ata ctg gta aat gcg ata 609
302 Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn Ala Ile
303         135               140               145
305 gca aaa gca gga aca aag cca gta caa cta gga caa cta ctc aac gtg 657
307 Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu Asn Val
308         150               155               160
310 tgc acc aca aat gcc tta tcg agg gtg atg cta ggg aag cga gtt ctc 705
311 Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg Val Leu
312         165               170               175
314 ggt gat ggc aca ggg aaa agc gac cca aaa gcc gag gaa ttt aag gac 753
316 Gly Asp Gly Thr Gly Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Asp
317 180               185               190
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319 atg gtg ctg gag tta atg gtt ctc acc gga gtt ttt aac att ggc gat 801
320 Met Val Leu Glu Leu Met Val Leu Thr Gly Val Phe Asn Ile Gly Asp

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VERIFICATION SUMMARY

DATE: 09/19/2001

PATENT APPLICATION: US/09/142,108B

TIME: 10:35:16

Input Set : A:\11658.bk1

Output Set: N:\CRF3\09192001\I142108B.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:398 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:989 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:993 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:997 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:2851 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
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VERIFICATION SUMMARY

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L:3348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:3378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45